CLAIM AMENDMENTS

Claims 1-6 (canceled)

7. (currently amended) An isolated nucleic acid molecule 20-51039 contiguous nucleotides in length consisting of a reverse or forward strand of a region of SEQ ID NO:4, wherein said region is selected from the group consisting of a 5'-non coding region depicted in nucleotides 51039-41739 of SEDQ ID NO:4, a 3'-non-coding region depicted in nucleotides 9503-1 of SEQ ID NO:4, a contiguous intron-exon region between nucleotides 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, ~~a and~~ contiguous exon-intron region between nucleotide 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, an intron depicted in nucleotides 36385-40645, 36309-33127, 32994-29616, 29564-25577, 25507-25384, 25287-21169, 21006-14110, 13953-13267, and/or 13188-10665, ~~or an isolated nucleic acid molecule of 20-51039 nucleotides in length consisting of a reverse or forward strand of a region of SEQ ID NO:4 or its reverse strand that comprises~~ a region comprising a dinucleotide of the following group: 41739-41738, 40645-40646, 36309-36310, 36384-36385, 32994-32995, 33126-33127, 29564-29565, 29615-29616, 25507-25508, 25287-25288, 25383-25384, 25576-25577, 21006-21007, 21168-21169, 14109-14110, 13953-13954, 13266-13267, 13188-13189, 10664-10665 and/or 9504-9503; a transcription binding site selected from the group consisting of

BINDING SITES	huMDM2, location in SEQ ID NO:4
AP1_C:	36-46, 2876-2886;
AP4_Q5:	7944-7980;
AP4_Q6:	7943-59, 8924-8940, 9294-9310;
ARNT_01:	1682-1706, 2193-2217, 9201-9225;
BRN2_01:	1040-1058, 7803-7821;
CAAT_01:	3292-3306;

CDPCR3HD_01: 6522-6540;

CEBPB_01: 1424-1438, 3917-3931, 4178-4192, 4787-4801, 6855-6869;

CREL_01: 5630-5642;

DELTAEF1_01: 83-95, 6328-6340;

FREAC7_01: 2757-2773, 5154-5170, 5823-5839;

GATA1_04: 4846-4858, 7017-7029;

GATA1_05: 8464-8476;

GATA2_02: 6045-6057, 6073-6085, 6142-6154;

GATA2_03: 2489-2501, 3323-3335, 3384-3396, 7393-7405;

GATA3_02: 3264-3276, 6870-6882;

GATA3_03: 40-52, 5729-5741, 6529-6541, 6874-6886, 7041-7053, 7589-7601;

GATA_C: 7 349-7361, 8188-8200;

HFH2_01: 1743-1759, 7995-8011;

HFH3_01: 502-518, 1739-1755, 4160-4176, 9402-9418, 9418-9434;

HFH8_01: 8184-8200;

IK2_01: 951-963, 3588-3600;

MZF1_01: 1202-1210, 1447-1455, 4997-4005, 5424-5432;

NF1_Q6: 1480-1500, 8166-8182;

NFAT_Q6: 4190-4208, 6009-6027;

NKX25_01: 741-755, 1648-1662, 1885-1899, 1984-1998, 3609-3623, 4928-4942, 5060-5074, 5889-5903, 8850-8864, 9190-9204;

NKX25_02: 2584-2599, 2970-2984, 4644-4658, 5179-5193, 6482-6496;

NMYC_01: 2560-2572;

RORA1_01: 220-238, 2638-2656;

S8_01: 4644-4656, 4842-4854, 4845-4857, 5200-5212, 5371-5383, 5735-5747, 6482-6494, 6541-6553, 6544-6556, 6772-6784, 7270-7292, 7273-7285;

SOX5_01: 1355-1371, 1430-1446, 3094-3110, 3155-3171, 4669-4685, 4692-4708,

4789-4805;

SRY_02: 4164-4180, 5665-5681;

TATA_01: 1261-1277, 2574-2590, 2723-2739, 2733-2749, 2770-2786, 4199-4215, 4206-4222;

TATA_C: 5900-5916, 7456-7472, 7702-7718, 7917-7933; and

XFD2_01: 7702-7218, 7917-7933; ,

a transcription binding site selected from the group consisting of

BINDING SITES huMDM2, location in SEQ ID NO:4

AP1_C: 12109-12119, 12695-12705, 22600-22610, 24166-24176, 31311-31321, 35234-35244, 39184-39194;

AP1_Q2: 11952-11962, 12068-12078, 14798-14808, 21748-21758, 22613-22623, 23676-23686, 26562-26572, 30046-30056;

AP1_Q4: 12695-12705, 31311-31321, 35234-35244, 36295-36305, 38784-38794, 39188-39198;

AP4_Q6: 31635-31651;

BRN2_01: 13448-13466, 14764-14782, 28094-28112, 40027-40045;

CAAT_01: 11288-11302, 15054-15068;

CDPCR3HD_01: 11286-11304, 13284-13302, 20846-20864, 29344-29362;

CEBPB_01: 29241-29255;

CREL_01: 36091-36103, 38873-38885;

DELTAEF1_01: 18083-18095, 20385-20397, 26955-26967;

FREAC7_01: 11982-11998, 15187-15202, 16523-16539, 16529-16545, 16587-16603, 16604-16620, 16676-16642, 16633-16649, 16644-16660, 16650-16666, 16657-16673, 16673-16689, 16762-16778, 21332-21348, 25689-25700, 26529-26545, 27767-27783, 29495-29511;

GATA1_02: 10916-10928, 15775-15789, 18162-18174, 26088-26100, 32518-32530;

GATA1_03: 28012-28024;

GATA1_04: 11153-11165, 11630-11642, 13778-13790, 17439-17451, 19300-19312, 21606-21618, 22743-22755, 23747-23759, 25806-25818, 26529-26541, 29424-29436, 30455-30467, 32761-32778, 33352-33364, 33960-33972, 36101-36113, 40007-40019;

GATA1_05: 11590-11602, 26550-26562, 36737-36749;

GATA1_06: 18772-18784, 23054-23066, 35568-35580, 37855-37867;

GATA2_02: 20755-20767, 30830-30842, 34755-34767, 36285-36297, 39143-39155, 39641-39653, 40586-40598;

GATA2_03: 13535-13547, 22711-22723, 23161-23173, 25028-25040, 27237-27249, 36277-36289;

GATA3_02: 11558-11570, 16470-16482, 17225-17237, 19619- 19631, 22156-22168, 22443-22455, 24713-24725, 27619-27631, 32716-32728, 34124-34136, 34163-34175, 36832-36844, 38403-38415;

GATA3_03: 10869-10881, 11515-11527, 13845-13857, 17221-17233, 18952-18964, 20050-20062, 40171-40183;

GATA_C: 15848-15860, 18899-18911, 23640-23652, 29072-29084, 30881-30893, 33198-33210, 37472-37484, 38621-38633;

GFI1_01: 35469-35481, 35492-35504;

HFH2_01: 15939-15955, 24636-24652, 25866-25882, 32171-32187, 35372-35388, 39457-35473;

HFH3_01: 13340-13356, 19218-19234, 21328-21344, 21336-21352, 21344-21360, 28062-28078, 32125-32141;

HFH8_01: 14133-14149, 22578-22584;

HNF3B_01: 13150-13166, 16505-16521, 25264-25280, 29443-29459, 37654-37670;

IK2_01: 11547-11559, 17144-17156, 18961-18973, 23883-23895, 27617-27629, 28908-28920, 29241-29253, 30752-30764, 34768-34780;

LYF1_01: 12319-12331, 19191-19203, 37226-37238, 39430-39442;

MAX_01: 22974-22986, 33339-33351;

MZF1_01: 26105-26113, 35187-35195;

NF1_Q6: 12048-12064, 33334-33354;

NFAT_Q6: 13295-13313, 14157-14175, 14311-14329, 14414-14432, 18269-18287, 19326-19344, 20801-20819, 21177-21195, 22537-22555, 23861-23879, 25392-25410, 25879-25897, 27524-27542, 30636-30654, 30718-30736, 31525-31543, 33655-33673, 34726-34744, 34917-34535, 34990-35008, 35979-35997, 36479-36493, 36577-36595, 37154-37172, 40224-40242, 40365-40383;

NKX25_01: 12041-12055, 12340-12354, 12471-12485, 12742-12756, 12877-12891, 13849-13863, 18995-19009, 21440-21454, 21883-21897, 28426-28440, 30964-30978, 32033-32047, 32265-

32279;

NKX25_02: 10998-11012, 12711-12725, 14131-14145, 14726-14740, 16024-16038;

NMYC_01: 18753-18765, 18754-18766, 23076-23088, 30534-30546, 34400-34412;

RORA1_01: 13134-13152, 22966-22984, 24934-24952, 33341-33359, 34760-34778;

S8_01: 11000-11012, 11977-11989, 12048-12060, 12051-12063, 13747-13759, 13923-13935, 13926-13938, 14676-14688, 14679-14691, 16026-16038, 16313-16325, 16316-16328, 17515-17527, 20756-20768, 20759-20771, 23154-23166, 23157-23169, 25198-25210, 25201-25213, 26651-26663, 27508-27520, 27511-27523, 29450-29462, 29478-28490, 29775-29787, 29778-29790, 29813-29825, 29816-29828, 31329-31341, 31677-31689, 31680-31692, 31732-31744, 31735-31747, 36137-36149, 36140-36152, 36812-36824, 36815-36827, 37413-37425, 38679-38691, 39474-39486, 39477-39489;

SOX5_01: 27397-27413, 27572-27588, 28100-28116, 29230-29246, 29439-29455, 30690-30706, 31595-31611, 33871-33887, 34113-34129, 34624-34640, 37668-37684, 38582-38598, 39124-39140, 40410-40426;

SRY_02: 20016-20032, 22410-22426, 27329-27345, 29162-29178, 29499-29515, 30646-30662, 31503-31519, 35928-35944, 37324-37340;

TATA_01: 32722-32738, 32729-32745, 32807-32823, 33825-33841, 34120-34136, 35433-35449, 36593-36609;

TATA_C: 11015-11031, 11817-11833, 13635-13651, 14930-14946;

TCF11_01: 18543-18549, 22574-22580, 31281-31297, 31489-31505, 38754-38770;

USF_01: 23075-23087, 32577-32589;

VMYB_02: 11526-11538, 17384-17396, 18400-18412, 19549-19561, 22188-22200, 40486-40508 and

XFD2_01: 16620-16636, 18153-18169, 22102-22118, 23141-23157,

And a transcription binding site selected from the group consisting of

BINDING SITES

huMDM2, I location in SEQ ID NO:4

AP1_C: 44584-44594, 49069-49079;

AP1_Q2: 42174-42184, 45217-45227, 48422-48422, 50447-50457;

AP1_Q4: 42702-42712, 50806-50816;

AP4_Q6: 42117-42133, 42118-42134, 42244-42260, 45432-45448; 45433-45449, 46609-

46625;

BRN2_01: 42310-42328, 44022-44040, 47514-47532, 48900-48918, 48967-48985;

CAAT_01: 44866-44880;

CDPCR3HD_01: 45671-45689, 49219-49237;

CREL_01: 42437-42449, 49797-49809;

FREAC7_01: 47026-47042, 47292-47308, 47658-47674;

GATA1_02: 43482-43494, 48926-48938, 49284-49296;

GATA1_03: 47371-47383;

GATA1_04: 43054-43066, 43162-43162, 43967-43979, 45464-45476, 45916-45928, 47763-47775;

GATA1_05: 49319-49331, 49459-49471;

GATA1_06: 47590-47602;

GATA2_02: 42660-42672, 43475-43487;

GATA2_03: 43714-43726, 50948-50960;

GATA3_02: 49155-49167, 49844-49856;

GATA3_03: 42202-42214, 44810-44822, 48438-48450, 49136-49148, 49337-49349, 49869-49881;

GATA_C: 44011-44023, 45256-45268, 45823-45835, 47915-47927, 49201-49213, 49573-49585;

GFI1_01: 46606-46618, 47063-47075;

HFH3_01: 47030-47046, 47284-47300, 47288-47304;

IK2_01: 45275-45287;

LYF1_01: 44564-44576, 46991-47003, 49567-49579;

MAX_01: 43234-43246, 48726-48738;

MZF1_01: 41772-41780, 42290-42298, 42295-42303, 44507-44515, 45105-45113, 45203-45211, 49948-49956, 50774-50782;

NF1_Q6: 50209-50229;

NFAT_Q6: 42061-42079, 44418-44436, 46399-46417, 47974-47992, 49267-49285, 49964-

	49982, 50392-50410;
NKX25_01:	42394-42408, 43507-43521, 46115-46129;
RORA1_01:	45073-45091, 48718-48736;
S8_01:	43552-43564, 45214-45226, 47160-47172, 48419-48431, 49295-49307, 50379-50391;
SOX5_01:	43716-43732, 46351-46367, 47156-47172, 47774-47790, 47868-47884, 47974-47990, 48915-48931, 50323-50339;
TATA_01:	45588-45604, 47625-47641, 48026-48042, 48659-48675, 49056-49072, 49079-49095, 49152-49168;
TCF11_01:	49115-49131;
VMYB_02:	42010-42022, 42279-42291, 44651-44663; and
XFD2_01:	42870-42886, 42910-42926.

Claims 8-9 (canceled)

10. (previously presented) A composition comprising the nucleic acid molecule of claim 7 and a carrier.

Claim 11 (canceled)

12. (withdrawn) A method for modulating levels of human mouse double minute 2 homolog in a subject in need thereof comprising administering to said subject an amount of the nucleic acid molecule of claim 7 effective to modulate said human mouse double minute 2 homolog levels.

Claim 13 (canceled)

14. (withdrawn) A method for preventing, treating or ameliorating a medical condition, comprising administering to a subject an amount of the nucleic acid molecule of claim 7 effective to prevent, treat or ameliorate said medical condition.

15. (previously presented) A kit comprising the nucleic acid molecule of claim 7.

16. (previously presented) The kit according to claim 15, in which the nucleic acid molecule is labeled with a detectable substance.

17. (previously presented) A solid support comprising the nucleic acid molecule of claim 7.

18. (original) The solid support of claim 17 wherein said support is a microarray.

Claim 19 (canceled)

20. (currently amended) The solid support of claim 18, which further comprises a nucleic acid molecule encoding human mouse double minute 2 homolog, complementary sequence thereof or a portion of said nucleic acid molecule containing at least 20 contiguous nucleotides.

Claim 21 (canceled)

22. (withdrawn) A method of identifying variants of SEQ ID NO:4, or its complementary sequence, comprising
isolating genomic DNA from a subject and determining the presence or absence of a variant in said genomic DNA using the nucleic acid molecule of claim 7.

23. (withdrawn) A method for detecting the presence or absence of SEQ ID NO:4 or its complementary sequence in a sample, said method comprising (a) contacting the sample with the nucleic acid molecule of claim 7 and (b) determining whether the nucleic acid molecule binds to said nucleic acid sequence in the sample.

24. (currently amended) An isolated nucleic acid molecule 20-5000 contiguous nucleotides in length consisting of a reverse or forward strand of a contiguous exon-intron region between nucleotides 41738-9502 of SEQ ID NO:4, or contiguous intron-exon region between nucleotides

41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2 ~~or a contiguous intron-exon region of SEQ ID NO:4~~.

25. (currently amended) The isolated nucleic acid molecule of claim 24, wherein said nucleic acid molecule is 20-5000 contiguous nucleotides in length and comprises nucleotides 41739-41738, 40645-40646, 36309-36310, 36384-36385, 32994-32995, 33126-33127, 29564-29565, 29615-29616, 25507-25508, 25287-25288, 25383-25384, 25576-25577, 21006-21007, 21168-21169, 13953-13954, 14109-14110, 13188-13189, 13266-13267, 10664-10665 and/or 9504-9503 of SEQ ID NO:4 or their reverse strands.

Claims 26-29 (canceled)

30. (previously presented) A microarray comprising a plurality of the nucleic acid molecules of claim 7.

31. (currently amended) The microarray of claim 30 wherein said microarray further comprises a nucleic acid molecule encoding human mouse double minute 2 homolog, complementary sequence thereof or a portion of said nucleic acid molecule containing at least 20 contiguous nucleotides.

32. (previously presented) A method for detecting the presence of a nucleic acid sequence of SEQ ID NO:4 or its complementary sequence in a sample, said method comprising contacting the sample with the nucleic acid molecule of claim 7 and determining whether the nucleic acid molecule binds to said nucleic acid sequence in the sample.

33. (new) A method for detecting the nucleic acid molecule of claim 7 in a sample comprising (a) amplifying said nucleic acid molecule and (b) detecting the presence of the amplified nucleic acid molecule of (a).

34. (new) The method according to claim 33, wherein amplifying is carried out by

polymerase chain reaction.

35. (new) The method according to claim 33, wherein said detecting is carried out by (a) contacting the amplified nucleic acid molecule with a probe comprising at least 20 contiguous nucleotides that is complementary to the amplified nucleic acid molecule; and (b) detecting specific hybridization between the probe and the amplified nucleic acid molecule to thereby detect the said nucleic acid molecule.

36. (new) A method for detecting the presence of the nucleic acid molecule of claim 7 in a sample, comprising contacting the sample with a probe comprising at least 20 contiguous nucleotides that hybridizes to said nucleic acid molecule under stringent conditions and determining whether the polynucleotide probe binds to said nucleic acid molecule in the sample.

37. (new) A method for isolating the nucleic acid molecule of claim 7 comprising
(a) isolating genomic DNA from a subject;
(b) providing primers, probes and optionally polymerase and
(c) incubating (a) and (b) under conditions promoting the isolation of said nucleic acid molecule.

38. (new) A method for obtaining the nucleic acid molecule of claim 7, comprising chemically synthesizing said nucleic acid molecule.